



9116-829.ST25.txt
SEQUENCE LISTING

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<120> Hairless Protein-Interacting Partner Complexes And Methods
Thereof For The Beautification And/Or Improvement Of Mammalian
Skin

<130> 9423

<140> US 10/712,629

<141> 2003-11-13

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<170> PatentIn version 3.3

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<212> DNA

<213> Nucleotide sequence of HRT corresponding to the amino acid residue 490-1182 of the C-terminal portion of HR protein

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<211> 693

<212> PRT

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20 25 30

Gln Leu Glu Glu Glu Asp Ser Ser Ala Thr Ser Glu Glu Gly Gly Gly
35 40 45

Gly Pro Gly Pro Glu Ala Ser Leu Asn Lys Gly Leu Ala Lys His Leu
50 55 60

Leu Ser Gly Leu Gly Asp Arg Leu Cys Arg Leu Leu Arg Lys Glu Arg
65 70 75 80

Glu Ala Leu Ala Trp Ala Gln Arg Glu Gly Gln Gly Pro Ala Met Thr
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Glu Asp Ser Pro Gly Ile Pro His Cys Cys Ser Arg Cys His His Gly
 100 105 110
 Leu Phe Asn Thr His Trp Arg Cys Ser His Cys Ser His Arg Leu Cys
 115 120 125
 Val Ala Cys Gly Arg Ile Ala Gly Ala Gly Lys Asn Arg Glu Lys Thr
 130 135 140
 Gly Ser Gln Glu Gln His Thr Asp Asp Cys Ala Gln Glu Ala Gly His
 145 150 155 160
 Ala Ala Cys Ser Leu Ile Leu Thr Gln Phe Val Ser Ser Gln Ala Leu
 165 170 175
 Ala Glu Leu Ser Thr Val Met His Gln Ala Trp Ala Lys Phe Asp Ile
 180 185 190
 Arg Gly His Cys Phe Cys Gln Val Asp Ala Arg Val Trp Ala Pro Gly
 195 200 205
 Asp Gly Gly Gln Gln Lys Glu Pro Thr Glu Lys Thr Pro Pro Thr Pro
 210 215 220
 Gln Pro Ser Cys Asn Gly Asp Ser Asn Arg Thr Lys Asp Ile Lys Glu
 225 230 235 240
 Glu Thr Pro Asp Ser Thr Glu Ser Pro Ala Glu Asp Gly Ala Gly Arg
 245 250 255
 Ser Pro Leu Pro Cys Pro Ser Leu Cys Glu Leu Leu Ala Ser Thr Ala
 260 265 270
 Val Lys Leu Cys Leu Gly His Asp Arg Ile His Met Ala Phe Ala Pro
 275 280 285
 Val Thr Pro Ala Leu Pro Ser Asp Asp Arg Ile Thr Asn Ile Leu Asp
 290 295 300
 Ser Ile Ile Ala Gln Val Val Glu Arg Lys Ile Gln Glu Lys Ala Leu
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 Gly Pro Gly Leu Arg Ala Gly Ser Gly Leu Arg Lys Gly Leu Ser Leu
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Pro Leu Ser Pro Val Arg Thr Arg Leu Ser Pro Pro Gly Ala Leu Leu
 340 345 350
 Trp Leu Gln Glu Pro Arg Pro Lys His Gly Phe His Leu Phe Gln Glu
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 His Trp Arg Gln Gly Gln Pro Val Leu Val Ser Gly Ile Gln Lys Thr
 370 375 380
 Leu Arg Leu Ser Leu Trp Gly Met Glu Ala Leu Gly Thr Leu Gly Gly
 385 390 395 400
 Gln Val Gln Ser Leu Thr Ala Leu Gly Pro Pro Gln Pro Thr Asn Leu
 405 410 415
 Asp Ser Thr Ala Phe Trp Glu Gly Phe Ser His Pro Glu Thr Arg Pro
 420 425 430
 Lys Leu Asp Glu Gly Ser Val Leu Leu Leu His Arg Thr Leu Gly Asp
 435 440 445
 Lys Asp Ala Ser Arg Val Gln Asn Leu Val Ser Ser Leu Pro Leu Pro
 450 455 460
 Glu Tyr Cys Ala His Gln Gly Lys Leu Asn Leu Ala Ser Tyr Leu Pro
 465 470 475 480
 Leu Gly Leu Thr Leu His Pro Leu Glu Pro Gln Leu Trp Ala Ala Tyr
 485 490 495
 Gly Val Asn Ser His Arg Gly His Leu Gly Thr Lys Asn Leu Cys Val
 500 505 510
 Glu Val Ser Asp Leu Ile Ser Ile Leu Val His Ala Glu Ala Gln Leu
 515 520 525
 Pro Pro Trp Tyr Arg Ala Gln Lys Asp Phe Leu Ser Gly Leu Asp Gly
 530 535 540
 Glu Gly Leu Trp Ser Pro Gly Ser Gln Thr Ser Thr Val Trp His Val
 545 550 555 560
 Phe Arg Ala Gln Asp Ala Gln Arg Ile Arg Arg Phe Leu Gln Met Val
 565 570 575
 Cys Pro Ala Gly Ala Gly Thr Leu Glu Pro Gly Ala Pro Gly Ser Cys
 580 585 590

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Tyr Leu Asp Ala Gly Leu Arg Arg Arg Leu Arg Glu Glu Trp Gly Val
595 600 605

Ser Cys Trp Thr Leu Leu Gln Ala Pro Gly Glu Ala Val Leu Val Pro
610 615 620

Ala Gly Ala Pro His Gln Val Gln Gly Leu Val Ser Thr Ile Ser Val
625 630 635 640

Thr Gln His Phe Leu Ser Pro Glu Thr Ser Ala Leu Ser Ala Gln Leu
645 650 655

Cys His Gln Gly Ala Ser Leu Pro Pro Asp His Arg Met Leu Tyr Ala
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Gln Met Asp Arg Ala Val Phe Gln Ala Val Lys Ala Ala Val Gly Ala
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Leu Gln Glu Ala Lys
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